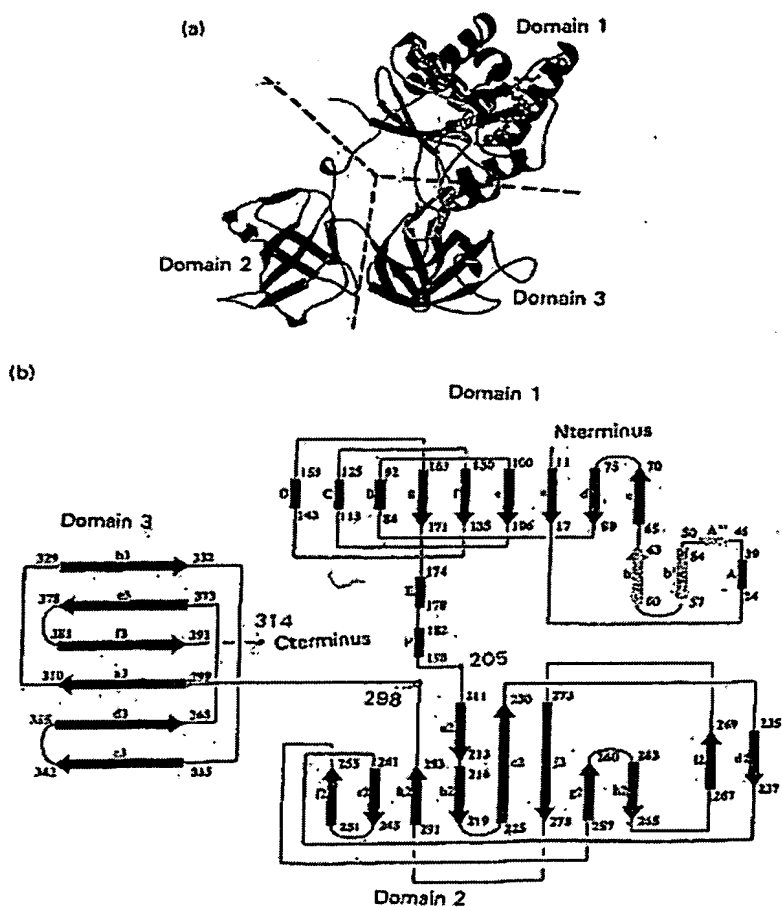


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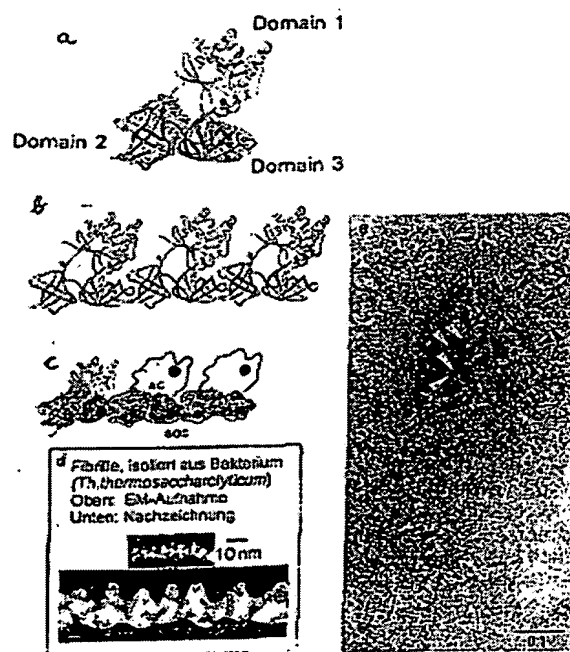
Figur 1



[Key to Figure 1:]

Figur = Figure

Figur 2



[Key to Figure 2:]

Figur = Figure

Fibrille, isoliert aus Bakterium = Fibrilla, isolated from the bacterium

Oben: EM-Aufnahme = Above: EM image

Unten: Nachzeichnung = Below: Copy

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Fig. 3

(a1)

Vektor pEGFP (Clontech):

```

      BsrGI      STOP      EcoRI
GAC GAG CTG TAC AAG TAA AGC GGC CGC GAC TCT AGA ATT CCA
CTG CTC GAC ATG TTC ATT TCG CCG GCG CTG AGA TCT TAA GGT

```

BsrGI-Schnittstelle:

```

T  GTACA
ACATG T

```

EcoRI-Schnittstelle:

```

G  AATTC
CTTAA G

```

Synthetisch hergestelltes Oligonukleotid zur Einklonierung des His-Tags in den Vektor:

```

5' BsrGI      BsrGI      EcoRI 3'
G TAC AAG CTT CAT CAC CAT CAC CAT CAC TAA CTG TAC AAG TAAG
      TTC GAA GTA GTG GTA GTG GTA GTG ATT GAC ATG TTC ATTCTTAA
3'
Tyr-Lys-Leu-His-His-His-His-His-His-STOP-

```

Ergebnis: pEGFP(His)

(a2)

Vektor pEGFP(His):

```

GCC TGC AGG -t- ACC ATG GTG
CGG ACG TCC -t- TGG TAC CAC

```

PstI-Schnittstelle:

```

CTGCA G
G  ACGTC

```

NcoI-Schnittstelle:

```

C  CATGG
GGTAC C

```

Fusionsstellen zum EF-Tu-Gen:

```

      Start EF-Tu      Start EGFP
5' PstI      HindIII  NcoI 3'
ACT AGC TGC AGC ATG TCT AAA -t- CTG GGC AAG CTT ACC ATG GTG
TGA TCG ACG TCG TAC AGA TTT -t- GAC CCG TTC GAA TGG TAC CAC
3'
Thr-Ser-Cys-Ser-Met-Ser-Lys-----Leu-Gly-Lys-Leu- Thr-Met-Val

```

[Key to Figure 3:]

Vektor = Vector

Schnittstelle = Interface

Synthetisch hergestelltes Oligonukleotid zur Einklonierung des His-Tags in den Vektor =

Synthetically produced oligonucleotide for cloning the His tag in the vector

Ergebnis = Result

Fusionsstellen zum EF-Tu-Gen = Fusion points in the EF-Tu gene

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(a3)

Fusionsstellen zur Domäne 3:

```

5'      PstI      Cys HindIII      NotI      3'
ACT AGC TGC AGC GCT AAG CCG -3- CTC GGC TGC AAG CTT ACC ATG GTG
TGA TCG ACC TCG CGA TTC GGC -3- GAC CCG ACG TTC GAA TGG TAC CAC
3'
Thr-Ser-Cys-Ser-Ala-Lys-Pro-----Leu-Gly-Cys-Lys-Leu-Thr-Met-Val

```

[Key to 4/15:]

Fusionsstellen zum Domäne 3 = Fusion points in domain 3

5'-TGAACA AAGGCGAGGA GCTGTTCAAC GGGTGGTGC CCATCCTGGT CGAGCTGGAC GGGGAGTAA ACGGCCACAA

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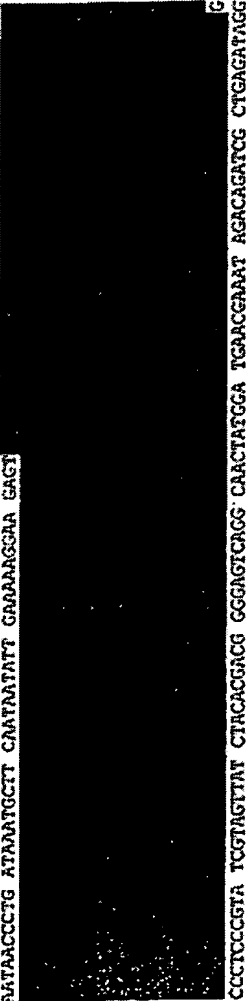
CTTCAGCTG TCCGGGAGG GCGAGGCGA TCCACCTAC GGCAGCTGA CCGTGMAGT CATCTGCACC ACCGGCAGC
TCCCGTGCC CTGGCCACC CTCTGACCA CCGCTGACG TCGCTTCAGCC GCTACCCCGA CCACATGNAG
CAGCAGACT TCTTCAGTC CCGCATGCC GAAGCTACG TCCAGAGCG CACCATCTTC TTCAGGAGC AGGCGACTA
CAGACCCGC CCGAGGTGA AGTTGAGGG CCGACCTC GTGACCGCA TCGAGCTGA GGCATCGAC TTCNAGGAGG
ACGCGACAT CCTGGGCGC AGCTGAGT ACATACAA CAGCCACAC GTCTATATCA TGGCCGACAA CCGAGAGAC
GCGATCAGG TGAATTCAG GATCGGCGC AGCATCGAG AGGCTGCGC CACCATGAC AGCGAGACAC
CCCATCGCC GCGGCGCG TGTGCTGCC CAGACGAC TACTGAGCA CCGAGTCCG CCGAGCAGG GACCCGACG
AGACCGCGA TCAATGCTC CTGCTGAGT TGTGACCG CCGCGGNTC ACTCTGCGA TCGCGAGGCTGAG

HLs-Tag:

CTTCATCAC ATCAACATCA CTACTGTATAC AAGTACATGAG

pEGFP-Vektor:

CAACTGAGCG CCGTGGCTA CCAATACCA CTCTGTCTGT GTCAAAATA ATAGGCTAC TAGTGGCGG TACGGCCCT
TTGTTCTCG CCGTTTUGT GATGACGCTG AATCTCTG ACATATGAG CTCCGAGCA CGGTACAGC TTCTCTGTA
GGGATGCGG GAGGAGACA AGCGGTGAG CCGGTGTCG GCGTGTGCG GCGTGTGTA ACTATGCGG
ATCAGAGCG ATTCTACTCA GACTGCACCA TATCGCTGT GAATACCGC ACAGTGGCT AGGAGGAAA TACCGCATCA
GGCGGCTTA AGGGCTGT GATACGCTA TTTTATAGG TTAATGTCAI GNTATATAG GTTCTTAGA CGTGAGGTG
CACTTTTCG GGAATGTG GCGGACCC TATTTGTTA TTTTCTAAA TACATTCBA TATGTATCG CTCATGAGC
ATAACCTG ATANTGCTI CAATATNTT GAAAGGAAA GAGT



CCCTCCCGTA TCGTAGTTAT CTACAGCG GGGGTGAGS CAATATGCA TGAAGAAAT AGACAGATCG CTGAGATAGG

[Key to 6/15:]

Vektor = Vector

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TGCCTCACTG ATTACGATT GGTACACGTC AGACCAAGTT TACTCATATA TACTTAGAT TCATTATATA CTCCTTTT
 AATTAAAG GATCTAGGTG AGATCCTTT TTGATAATCT CAGACCAAA ATCCCTTAC GTCGTTC GTCCACTGA
 GGTACAGACC CC
 [REDACTED]
 GGCC TTTCCTGGC CTTTGTCTCA CAGTTCCTT CCGCTGTTT CCCTGATTC TGTGGATAC
 CGATTACCG CTTTCAGTG AGCTGATACC GTCGCGCA GCGACGAC CAGGCCAGC GATCTAGTA GCGAGGAGC
 CGAAG

Sequenz 2 Lac-Promotor

Sequenz 3 Lac-Operator

Sequenz 4 Ribosomen-Bindungsstelle

Sequenz 5 Ampicillin-Resistenz-Gen

Sequenz 6 pUC Plasmid-Replikations-Origin

1. NotI
 2. XbaI
 3. BstXI
 4. EcoRI

[Key to 7/15:]

Sequenz: Lac-Promotor = Sequence: Lac-promoter

Ribosomen-Bindungsstelle = Ribosome binding site

Ampicillin-Resistenz-Gen = Ampicillin resistance gene

Klonierungsstellen = Cloning sites

The sequence contains four silent mutations () that are clearly present according to sequence analysis:

(1) To be: TAT, Is: TA -> Tyr; codon usage (entire E. coli genome) is changed from 16.2 to 12.2

(2) To be: TAC, Is: TA -> Tyr; codon usage (entire E. coli genome) is changed from 12.2 to 16.2

(3) To be: GCA, Is: GC -> Ala; codon usage (entire E. coli genome) is changed from 20.1 to 33.6

(4) To be: ATT, Is: AT -> Ile; codon usage (entire E. coli genome) is changed from 30.3 to 25.1 (frequency per thousand)

Sequenz des Konstrukts Domäne 3 von EF-Tu-GFP-His im Vektor pEGFP (Clontech) (SEQ ID NO:2)
(b2)

pEGFP-Vektor:

AGCGCCCAAT ACGCAACCG CCTCTCCCG CGGTTGSCC GATTCATPAA TGCAGCTGC ACACAGGTT TCCGACTGG
AAGCGGGCA ~~ATGAGCGCA ACGGCTGCTT TTTTCTGCTGCTT TTTTCTGCTGCTT TTTTCTGCTGCTT~~
~~ATGAGCGCA ACGGCTGCTT TTTTCTGCTGCTT TTTTCTGCTGCTT TTTTCTGCTGCTT~~
CATGCGGCGAGC

Domäne 3 von EF-Tu:

GCTAAGCCGG GCACCATCAA GCGGCACACC AAGTTGANT CTGAGTGTA CATTCGTCC AAGATGAAG GCGGCCGTCA
TACTCCGTTC TTCRAAGGCT ACGGTCCGCA GTTCTACTTC CGTACTACTG ACGTGACTGG TACCATGAA CTGCCGGAAG
CGGTAGAGAT GGTATGCCG GGCACACACA TCAAAATGGT TGTATCCCTG ATCCACCGA TCGGATGGA CGACGCTCTG
CGTTTGGCA TCCGTGAAG GCGCCGTACC GTTGGCGCGG GCGTTGTAGC TAAGTTCTG GCGTGC

pEGFP-Vektor:

AAGCTTACG

GFP:

~~ATGAGCGCA ACGGCTGCTT TTTTCTGCTGCTT TTTTCTGCTGCTT TTTTCTGCTGCTT~~
ATGAGCGCA ACGGCTGCTT TTTTCTGCTGCTT TTTTCTGCTGCTT TTTTCTGCTGCTT
GTTCAAGCTG TCCGGCGAGG GCGAGGGCGA TGCACCTAC GGCAGCTGA CCTGAAGTT CATTCGACC ACGGCAAGC
TGCCCGTGCC CTGGCCCAAC CTGCTGACCA CCTGACCTA CGGCTGCGAG TCGTTACGCC GCTACCCGA CCACATGAAG
CAGACGACT TCTTCAAGTC CGCATGCCG GAAGGCTACG TCCAGGAGCG CACCATCTTC TTCAGGAGG ACGGCAACTA
CAGACCCCG CCGGAGGTGA AGTTGAGGG CGACACCTG GTGACCCGA TCGGCTGTA GGCATGAC TTCAGGAGG
ACGGCAACAT CCTGGGGCAC AAGTTGAGT ACACCTACA CAGGCAAC CAGGCAAC TGGCCGACA GCGAGAAC
GGCATCAAGG TGAACCTTCAA GATCCGCCAC AACATCGAGG ACGGCAAGG GACGCTGCC GACCATCTAC AGCAGAAC
CCCATCGGC GACGGCCCG TGTGCTGCC GACCAACAC TACCTGAGCA CCGAGTCCG CCGAGGCAA GACCCACG
AGAGCGCGA TCACATGGTC CTGCTGGAGT TCGTGACCG CCGCGGATC ACTCTGGCA TGGACGAGT ~~ATGAGCGCA~~

His-Tag:

CTTCATCACC ATCACCATCA CTAACTGTAC AAGTAAG ~~ATGAGCGCA~~

[Key to 9/15:]

Sequenz des Konstrukts Domäne 3 von EF-Tu-GFP-His im Vektor pEGFP (Clontech) (SEQ ID

No: 2) (b2) = Sequence of the domain-3 construct of EF-Tu-GFP-His in the vector

pEGFP (Clontech) (SEQ ID No: 2) (b2)

Vektor = Vector

Domäne = Domain

pEGFP-Vektor:

CAACTGAGCG CCGGTCCGTA CCATTACCAA CTTGTCTGGT GTCAAAATA ATAGCCTAC TAGTCGGCCG TACGGCCCT
TTCTCTCCG GCGTTTCGGT GATGACGGTG AAAACCTCTG ACACATCCAG CTCCTGGAGA CCGTCACAGC TTGTCGTGTA
GCGGATCCCG GGAGCAGRCA AGCCCGTCAG GCGCGTCAG CCGGTGTGG GGTGGCTTA ACTATGCCGC
ATCAGAGCAG ATTGTACTGA GAGTGCACCA TATGGGGTGT GAAATACCGC ACAGATCCGT AAGGAGRAA TACCGCATCA
GGCGGCTTA AGGCTCTCGT GATACGGCTA TTTTATAGG TTAATGTCAT GATAATATG GTTCTTAGA CGTCAGGTGG
CACTTTTCGG GGAATGTC GCGGAACCC TATTTGTTA TTTTCTRA TACATTCAA TATGTATCCG CTCATGAGAC
AATACCCG ATAAATGCTT CAATATATT GAAAGGAA GAGT

CCCTCCGTA TCGTAGTAT CTACACGACG GGGAGTCAGG CAACTATGGA TGAACGAAAT AGACAGATCG CTGAGATAGG
TGCTCACTG ATTAGCATT GGTAACTGTC AGACCAAGTT TACTCATATA TACTTTAGAT TGATTAAAA CTCATTTT
AATTTAAAG GATCTAGGTG AGATCCTTT TTGATATCT CATGACCATA ATCCCTTAAAC GTGAGTTTC GTTCCACTGA
GGTCAGACC CC

[Key to 10/15:]

Vektor = Vector

GGCC TTTTGCTGGC CTTTGCTCA CATGTTCTTT CCTGGTTAT CCGTGATTC TGTGGATAC
CGATTACCG CCTTGAGTG AGCTGATACC GCTGCGCCGA GCGGACGAC CGAGCGCAGC GAGTCAGTGA GCGGGAAGC
GGAC

Sequenz Lac-Promotor

Sequenz Lac-Operator

Sequenz Ribosomen-Bindungsstelle

Sequenz Ampicillin-Resistenz-Gen

Sequenz pUC Plasmid-Replikations-Origin

Restriktionsenzyme

5.	GTAAC	PstI
6.	GAATC	NcoI
7.	ATGAC	BsrCI
8.	GAATC	EcoRI

Die Sequenz enthält eine silent mutation (**ATG**), die laut Sequenzanalyse eindeutig vorhanden ist:

Soll: ATT, Ist: AT**G** -> Ile; Codon usage (gesamtes Genom E. coli) ändert sich von 30,3 zu 25,1 (Frequenz pro Tausend)

[Key to 11/15:]

Sequenz: Lac-Promotor = Sequence: Lac-promoter

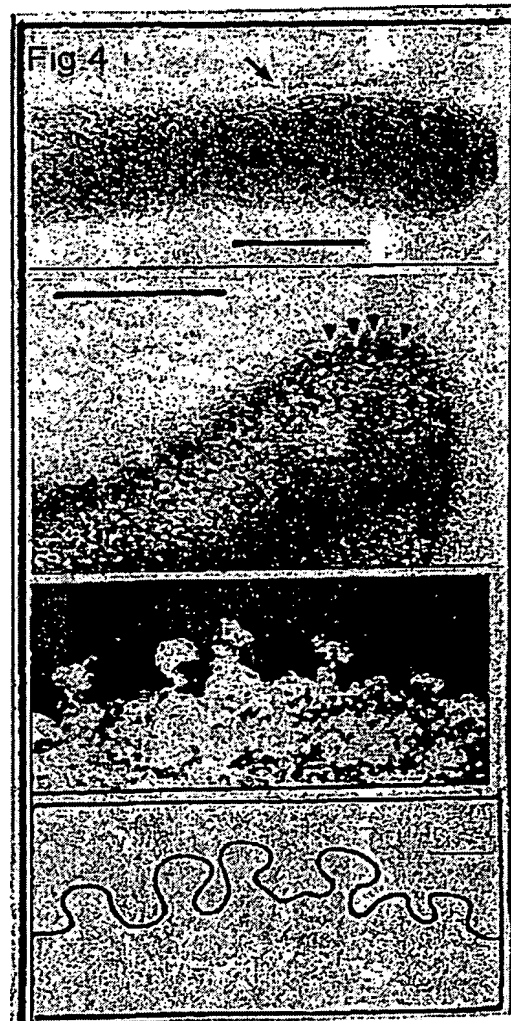
Ribosomen-Bindungsstelle = Ribosome binding site

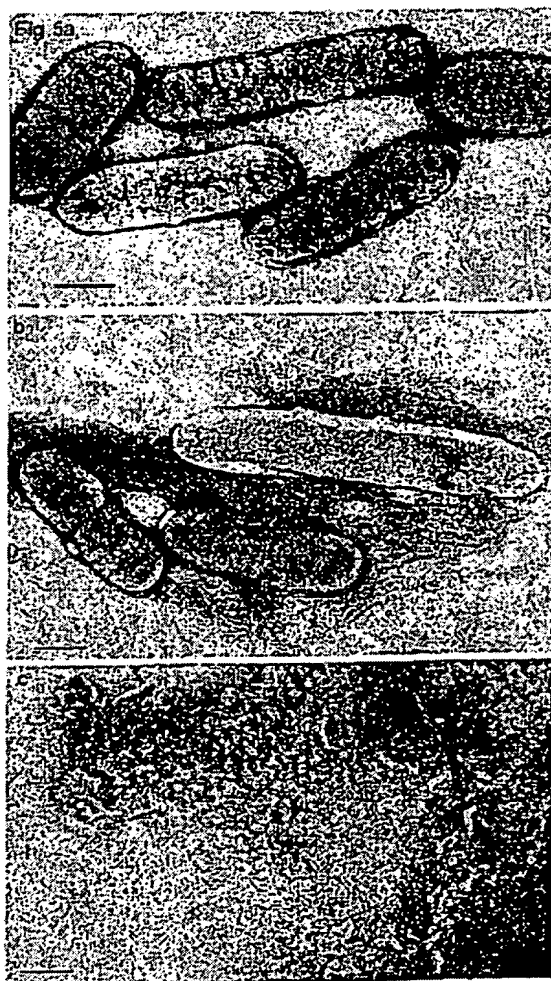
Ampicillin-Resistenz-Gen = Ampicillin resistance gene

Klonierungsstellen = Cloning Sites

[last sentence:] The sequence contains a silent mutation (), which is clearly present according to the sequence analysis:

To be: ATT, Is: AT -> Ile; codon usage (entire E. coli genome) is changed from 30.3 to 25.1 (frequency per thousand)

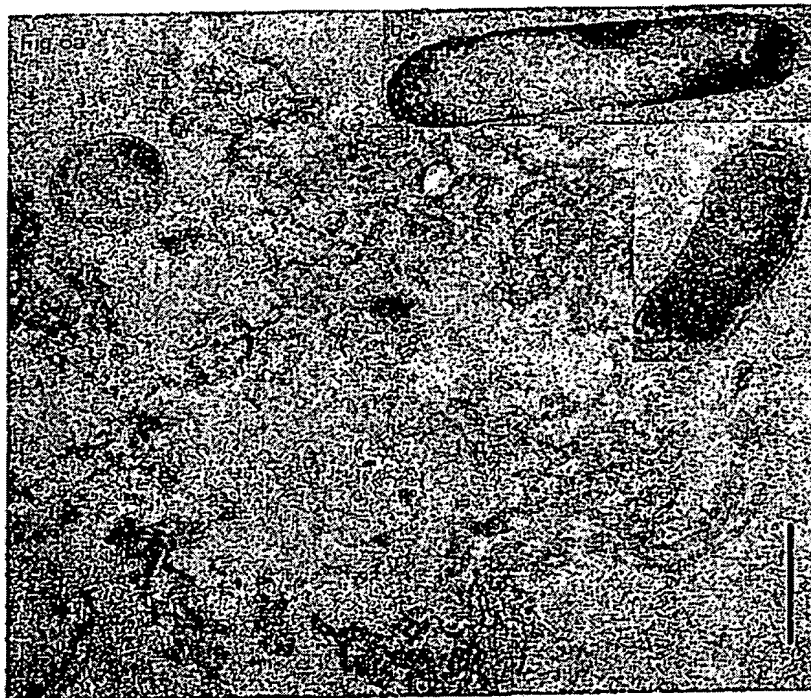




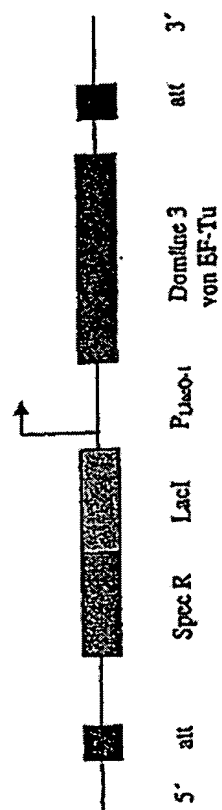
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Figur 7



[Key to Figure 7:]

Figur = Figure

Domäne 3 von EF-Tu = Domain 3 of EF-Tu

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